

Claims:

5 1. In a method for improving the expression of a heterologous gene in plants by modifying the structural coding sequence of said gene, the improvement which comprises reducing the occurrence of polyadenylation signals selected from the group consisting of AATAAA, AATAAT, AACCAA, ATATAA, AATCAA,
10 ATACTA, ATAAAA, ATGAAA, AAGCAT, ATTAAT, ATACAT, AAAATA, ATTAAA, AATTAA, AATACA and CATAAA.

2. The method of Claim 1 further comprising the improvement of reducing the occurrence of ATTTA sequences within the structural coding sequence.

15 3. A method for modifying a wild-type structural gene sequence which encodes an insecticidal protein of *Bacillus thuringiensis* to enhance the expression of said protein in plants which comprises:

- 20 a) removing polyadenylation signals contained in said wild-type gene while retaining a sequence which encodes said protein; and
- b) removing ATTTA sequences contained in said wild-type gene while retaining a sequence which encodes said protein.

25 4. A method of Claim 3 further comprising the removal of self-complementary sequences and replacement of such sequences with nonself-complementary DNA comprising plant preferred codons while retaining a structural gene sequence encoding said protein.

30 5. A method of Claim 4 further comprising the use of plant preferred sequences in the removal of the polyadenylation signals and ATTTA sequences.

5 6. A method of Claim 3 in which the polyadenylation signals are selected from the group consisting of AATAAA, AATAAT, AACCAA, ATATAA, AATCAA, ATACTA, ATAAAA, ATGAAA, AAGCAT, ATTAAT, ATACAT, AAAATA, ATTAAA, AATTAA, AATACA and CATAAA.

10 7. A method of Claim 4 in which the polyadenylation signals are selected from the group consisting of AATAAA, AATAAT, AACCAA, ATATAA, AATCAA, ATACTA, ATAAAA, ATGAAA, AAGCAT, ATTAAT, ATACAT, AAAATA, ATTAAA, AATTAA, AATACA and CATAAA.

15 8. A method of Claim 5 in which the polyadenylation signals are selected from the group consisting of AATAAA, AATAAT, AACCAA, ATATAA, AATCAA, ATACTA, ATAAAA, ATGAAA, AAGCAT, ATTAAT, ATACAT, AAAATA, ATTAAA, AATTAA, AATACA and CATAAA.

20 9. A method for modifying a wild-type structural gene sequence which encodes an insecticidal protein of *Bacillus thuringiensis* to enhance the expression of said protein in plants which comprises:

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- a) identifying regions within said sequence with greater than four consecutive adenine or thymine nucleotides;
 - b) modifying the regions of step (a) which have two or more polyadenylation signals within a ten base sequence to remove said signals while maintaining a gene sequence which encodes said protein; and
 - c) modifying the 15-30 base regions surrounding the regions of step (a) to remove major plant polyadenylation signals, consecutive sequences containing more than one minor polyadenylation
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signal and consecutive sequences containing more than one ATTTA sequence while maintaining a gene sequence which encodes said protein.

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10. A method of Claim 9 in which the major plant polyadenylation signals are selected from the group consisting of AATAAA and AATAAT.

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11. A method of Claim 10 in which the polyadenylation signals are selected from the group consisting of AATAAA, AATAAT, AACCAA, ATATAA, AATCAA, ATACTA, ATAAAA, ATGAAA, AAGCAT, ATTAAT, ATACAT, AAAATA, ATTAAA, AATTAA, AATACA and CATAAA.

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12. A method of Claim 11 further comprising the use of plant preferred sequences in the removal of polyadenylation signals and ATTTA sequences.

13. A structural gene which encodes an insecticidal protein of *Bacillus thuringiensis*, said gene being substantially devoid of polyadenylation signals and ATTTA sequences.

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14. A structural gene of Claim 13 which is substantially devoid of polyadenylation signals selected from the group consisting of AATAAA, AATAAT, AACCAA, ATATAA, AATCAA, ATACTA, ATAAAA, ATGAAA, AAGCAT, ATTAAT, ATACAT, AAAATA, ATTAAA, AATTAA, AATACA and CATAAA.

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15. A structural gene of Claim 13 which encodes an insecticidal protein of *B.t.k.* HD-1 having the sequence:

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1 ATGGCTATAGAACTGGTTACACCCCAATCGATATTTCT 40
41 TGTCGCTAACGCAATTTCTTTTGAGTGAATTTGTTCCCGG 80
10 81 TGCTGGATTTGTGTTAGGACTAGTTGATATTATCTGGGGA 120
121 ATTTTGGTCCCTCTCAATGGGACGCATTTCTTGTAACA 160
161 TTGAACAGCTCATCAACCAGAGAATCGAAGAGTTCGCTAG 200
15 201 GAATCAAGCCATTTCTAGATTAGAAGGACTAAGCAATCTT 240
241 TATCAAATTTACGCAGAATCTTTTAGAGAGTGGAAGCAG 280
20 281 ATCCTACTAATCCAGCATTAAGAGAAGAGATGCGTATTCA 320
321 ATTCAATGACATGAACAGTGCCCTTACAACCGCTATTCCT 360
361 CTTTTGCAGTTCAAATTAATCAAGTTCCTCTCCTCTCCG 400
25 401 TGTACGTTCAAGCTGCCAACCTCCACCTCTCAGTTTTGAG 440
441 AGATGTTTCAGTGTTTGGACAAAGGTGGGGATTTGATGCC 480
481 GCGACTATCAATAGTCGTTATAATGATTTAACTAGGCTTA 520
30

521 TTGGCAACTATACAGATCATGCTGTACGCTGGTACAATAC 560
5 561 GGGATTAGAGCGTGTATGGGGACCGGATTCTAGAGATTGG 600
601 ATCAGGTACAACCAGTTCAGAAGAGAGCTTACACTAACTG 640
641 TATTAGATATCGTTTCTCTATTTCCGAACCTATGATAGTAG 680
10 681 AACGTATCCAATTCGAACAGTTTCCCAATTAACAAGAGAA 720
721 ATTTATACAAACCCAGTATTAGAAAATTTTGATGGTAGTT 760
15 761 TTCGAGGCTCGGCTCAGGGCATAGAAGGAAGTATTAGGAG 800
801 TCCACATTTGATGGATATACTTAATAGTATAACCATCTAT 840
841 ACGGATGCTCATAGAGGAGAATACTACTGGTCCGGTCACC 880
20 881 AGATCATGGCTTCTCCTGTAGGGTTTTTCGGGGCCAGAATT 920
921 CACTTTTCCGCTATATGGAACCTATGGGAAATGCAGCTCCA 960
961 CAACAACGTATTGTTGCTCAACTAGGTCAGGGCGTGTATA 1000
25 1001 GAACATTATCGTCCACCTTATATAGAAGACCTTTTAACAT 1040
1041 CGGGATCAACAACCAACAACCTATCTGTTCTTGACGGGACA 1080
30 1081 GAATTTGCTTATGGAACCTCCTCAAATTTGCCATCCGCTG 1120

1121 TATACAGAAAAAGCGGAACGGTAGATTCGCTGGATGAAAT 1160
5 1161 ACCGCCACAGAATAACAACGTGCCACCTAGGCAAGGATTT 1200
1201 AGTCATCGATTAAGCCATGTTTCAATGTTTCGTTTCAGGCT 1240
1241 TTAGTAATAGTAGTGTAAGTATAATAAGAGCTCCTATGTT 1280
10 1281 CTCTTGGATACATCGTAGTGCTGAGTTCAACAACATCATC 1320
1321 CCTTCATCACAAATCACCCAAATCCCACTCACCAAGTCTA 1360
15 1361 CTAATCTTGGCTCTGGAACCTTCTGTCGTTAAAGGACCAGG 1400
1401 ATTTACAGGAGGAGATATTCTTCGAAGAACTTCACCTGGC 1440
1441 CAGATTTCAACCTTAAGAGTAAATATTACTGCACCATTAT 1480
20 1481 CACAAAGATATCGGGTAAGAATTCGCTACGCTTCTACCAC 1520
1521 AAACCTTCAGTTCCACACATCAATTGACGGAAGACCTATT 1560
1561 AATCAGGGGAATTTTTCAGCAACTATGAGTAGTGGGAGTA 1600
25 1601 ATTTACAGTCCGGAAGCTTTAGGACTGTAGGTTTTACTAC 1640
1641 TCCGTTTAACTTTTCAAATGGATCAAGTGATTTTACGTTA 1680
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1681 AGTGCTCATGTCTTCAATTCAGGCAATGAAGTTTATATAG 1720
5 1721 ATCGAATTGAATTTGTTCCGGCA 1743.

16. A structural gene of Claim 13 which encodes an insecticidal protein of *B.t.k.* HD-73 having the sequence:

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1 ATGGCCATTGAAACCGTTACACTCCCATCGACATCTCCT 40
41 TGTCTTGACACAGTTTCTGCTCAGCGAGTTCGTGCCAGG 80
15 81 TGCTGGGTTCGTTCTCGGACTAGTTGACATCATCTGGGGT 120
121 ATCTTTGGTCCATCTCAATGGGATGCATTCCTGGTGCAA 160
161 TTGAGCAGTTGATCAACCAGAGGATCGAAGAGTTCGCCAG 200
20 201 GAACCAGGCCATCTCTAGGTTGGAAGGATTGAGCAATCTC 240
241 TACCAAATCTATGCAGAGAGCTTCAGAGAGTGGGAAGCCG 280
25 281 ATCCTACTAACCCAGCTCTCCGCGAGGAAATGCGTATTCA 320
321 ATTCAACGACATGAACAGCGCCTTGACCACAGCTATCCCA 360
361 TTGTTGCGAGTCCAGAACTACCAAGTTCCTCTCTGTCCG 400
30 401 TGTACGTTCAAGCAGCTAATCTTCACCTCAGCGTGCTTCG 440

441 AGACGTTAGCGTGTTTGGGCAAAGGTGGGGATTTCGATGCT 480
5 481 GCAACCATCAATAGCCGTTACAACGACCTTACTAGGCTGA 520
521 TTGGAAACTACACCGACCACGCTGTTCGTTGGTACAACAC 560
561 TGGCTTGGAGCGTGTCTGGGGTCCCTGATTCTAGAGATTGG 600
10 601 ATTAGATACAACCAGTTCAGGAGAGAATTGACCCTCACAG 640
641 TTTTGGACATTGTGTCTCTCTTCCCGAACTATGACTCCAG 680
15 681 AACCTACCCTATCCGTACAGTGTCCCAACTTACCAGAGAA 720
721 ATCTATACTAACCCAGTTCCTTGAGAACTTCGACGGTAGCT 760
761 TCCGTGGTTCTGCCCCAAGGTATCGAAGGCTCCATCAGGAG 800
20 801 CCCACACTTGATGGACATCTTGAACAGCATAACTATCTAC 840
841 ACCGATGCTCACAGAGGAGAGTATTACTGGTCTGGACACC 880
881 AGATCATGGCCTCTCCAGTTGGATTTCAGCGGGCCCGAGTT 920
25 921 TACCTTTCCTCTCTATGGAACCTATGGGAAACGCCGCTCCA 960
961 CAACAACGTATCGTTGCTCAACTAGGTCAGGGTGTCTACA 1000
30 1001 GAACCTTGTCTTCCACCTTGATACAGAAGACCCTTCAATAT 1040

1041 CGGTATCAACAACCAGCAACTTTCCGTTCTTGACGGAACA 1080
5 1081 GAGTTCGCCTATGGAACCTCTTCTAACTTGCCATCCGCTG 1120
1121 TTTACAGAAAGAGCGGAACCGTTGATTCCCTGGACGAAAT 1160
1161 CCCACCACAGAACAACAATGTGCCACCCAGGCAAGGATTC 1200
10 1201 TCCCACAGGTTGAGCCACGTGTCCATGTTCCGTTCCGGAT 1240
1241 TCAGCAACAGTTCCGTGAGCATCATCAGAGCTCCTATGTT 1280
1281 CTCTTGGATACACCGTAGTGCTGAGTTCAACAACATCATC 1320
15 1321 GCATCCGATAGTATTACTCAAATCCCTGCAGTGAAGGGAA 1360
1361 ACTTTCTCTTCAACGGTTCTGTCAATTCAGGACCAGGATT 1400
20 1401 CACTGGTGGAGACCTCGTTAGACTCAACAGCAGTGGAAAT 1440
1441 AACATTCAGAATAGAGGGTATATTGAAGTTCCAATTCACT 1480
1481 TCCCATCCACATCTACCAGATATAGAGTTCGTGTGAGGTA 1520
25 1521 TGCTTCTGTGACCCCTATTACCTCAACGTTAATTGGGGT 1560
1561 AATTCATCCATCTTCTCCAATACAGTTCCAGCTACAGCTA 1600
30 1601 CCTCCTTGGATAATCTCCAATCCAGCGATTTCCGTTACTT 1640

1641 TGAAAGTGCCAATGCTTTTACATCTTCACTCGGTAACATC 1680
 5 1681 GTGGGTGTTAGAACTTTAGTGGGACTGCAGGAGTGATTA 1720
 1721 TCGACAGATTCGAGTTCATTCCAGTTACTGCAACACTCGA 1760
 1761 GGCTGAG 1767.

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17. A structural gene of Claim 13 encoding a
 insecticidal protein of *B.t.k.* HD-1 having the
 sequence:

15 1 ATGGACAACAACCCAAACATCAACGAATGCATTCCATACA 40
 41 ACTGCTTGAGTAACCCAGAAAGTTGAAGTACTTGGTGGAGA 80
 81 ACGCATTGAAACCGGTTACACTCCCATCGACATCTCCTTG 120
 20 121 TCCTTGACACAGTTTCTGCTCAGCGAGTTCGTGCCAGGTG 160
 161 CTGGGTTCGTTCTCGGACTAGTTGACATCATCTGGGGTAT 200
 201 CTTTGGTCCATCTCAATGGGATGCATTCTGGTGCAAATT 240
 25 241 GAGCAGTTGATCAACCAGAGGATCGAAGAGTTCGCCAGGA 280
 281 ACCAGGCCATCTCTAGGTTGGAAGGATTGAGCAATCTCTA 320
 30 321 CCAAATCTATGCAGAGAGCTTCAGAGAGTGGGAAGCCGAT 360

	361	CCTACTAACCCAGCTCTCCGCGAGGAAATGCGTATTCAAT	400
5	401	TCAACGACATGAACAGCGCCTTGACCACAGCTATCCCATT	440
	441	GTTTCGCAGTCCAGAACTACCAAGTTCCTCTCTTGTCCGTG	480
	481	TACGTTCAAGCAGCTAATCTTCACCTCAGCGTGCTTCGAG	520
10	521	ACGTTAGCGTGTTTGGGCAAAGGTGGGGATTTCGATGCTGC	560
	561	AACCATCAATAGCCGTTACAACGACCTTACTAGGCTGATT	600
15	601	GGAAACTACACCGACCACGCTGTTTCGTTGGTACAACACTG	640
	641	GCTTGGAGCGTGTCTGGGGTCCTGATTCTAGAGATTGGAT	680
	681	TAGATACAACCAGTTCAGGAGAGAATTGACCCTCACAGTT	720
20	721	TTGGACATTGTGTCTCTCTCCCGAACTATGACTCCAGAA	760
	761	CCTACCCTATCCGTACAGTGTCCCAACTTACCAGAGAAAT	800
	801	CTATACTAACCCAGTTCTTGAGAACTTCGACGGTAGCTTC	840
25	841	CGTGGTTCTGCCCAAGGTATCGAAGGCTCCATCAGGAGCC	880
	881	CACACTTGATGGACATCTTGAACAGCATAACTATCTACAC	920
30	921	CGATGCTCACAGAGGAGAGTATTACTGGTCTGGACACCAG	960

5 961 ATCATGGCCTCTCCAGTTGGATTGAGCGGGCCCGAGTTTA 1000
1001 CCTTTCCTCTCTATGGAACATATGGGAAACGCCGCTCCACA 1040
1041 ACAACGTATCGTTGCTCAACTAGGTCAGGGTGTCTACAGA 1080
1081 ACCTTGTCTTCCACCTTGTACAGAAGACCCTTCAATATCG 1120
10 1121 GTATCAACAACCAGCAACTTTCCGTTCTTGACGGAACAGA 1160
1161 GTTCGCCTATGGAACCTCTTCTAACTTGCCATCCGCTGTT 1200
15 1201 TACAGAAAGAGCGGAACCGTTGATTCCCTGGACGAAATCC 1240
1241 CACCACAGAACAACAATGTGCCACCCAGGCAAGGATTCTC 1280
1281 CCACAGGTTGAGCCACGTGTCCATGTTCCGTTCCGGATTCT 1320
20 1321 AGCAACAGTTCCGTGAGCATCATCAGAGCTCCTATGTTCT 1360
1361 CATGGATTCATCGTAGTGCTGAGTTCAACAATATCATTCC 1400
25 1401 TTCCTCTCAAATCACCCAAATCCCATTGACCAAGTCTACT 1440
1441 AACCTTGGATCTGGAACCTTCTGTCGTGAAAGGACCAGGCT 1480
1481 TCACAGGAGGTGATATTCTTAGAAGAACTTCTCCTGGCCA 1520
30 1521 GATTAGCACCCCTCAGAGTTAACATCACTGCACCACTTTCT 1560

1561 CAAAGATATCGTGTCTCAGGATTCGTTACGCATCTACCACTA 1600
5 1601 ACTTGCAATTCCACACCTCCATCGACGGAAGGCCTATCAA 1640
1641 TCAGGGTAACTTCTCCGCAACCATGTCAAGCGGCAGCAAC 1680
1681 TTGCAATCCGGCAGCTTCAGAACCGTCGGTTTCACTACTC 1720
10 1721 CTTTCAACTTCTCTAACGGATCAAGCGTTTTACCCCTTAG 1760
1761 CGCTCATGTGTTCAATTCTGGCAATGAAGTGACATTGAC 1800
15 1801 CGTATTGAGTTTGTGCCTGCCGAAGTTACCTTCGAGGCTG 1840
1841 AGTAC 1845. a

18. A structural gene of Claim 13 encoding an
20 insecticidal protein derived from *B.t.k.* HD-73 having
the sequence:

1 ATGGACAACAACCCAAACATCAACGAATGCATTCCATACA 40
25 41 ACTGCTTGAGTAACCCAGAAGTTGAAGTACTTGGTGGAGA 80
81 ACGCATTGAAACCGGTTACACTCCCATCGACATCTCCTTG 120
121 TCCTTGACACAGTTTCTGCTCAGCGAGTTCGTGCCAGGTG 160
30 161 CTGGGTTCGTTCTCGGACTAGTTGACATCATCTGGGGTAT 200

201 CTTTGGTCCATCTCAATGGGATGCATTCCTGGTGCAAATT 240
5 241 GAGCAGTTGATCAACCAGAGGATCGAAGAGTTCGCCAGGA 280
281 ACCAGGCCATCTCTAGGTTGGAAGGATTGAGCAATCTCTA 320
321 CCAAATCTATGCAGAGAGCTTCAGAGAGTGGGAAGCCGAT 360
10 361 CCTACTAACCCAGCTCTCCGCGAGGAAATGCGTATTCAAT 400
401 TCAACGACATGAACAGCGCCTTGACCACAGCTATCCCATT 440
15 441 GTTCGCAGTCCAGAACTACCAAGTTCCTCTCTTGTCCTGTG 480
481 TACGTTCAAGCAGCTAATCTTCACCTCAGCGTGCTTCGAG 520
521 ACGTTAGCGTGTTTGGGCAAAGGTGGGGATTTCGATGCTGC 560
20 561 AACCATCAATAGCCGTTACAACGACCTTACTAGGCTGATT 600
601 GGAAACTACACCGACCACGCTGTTCGTTGGTACAACACTG 640
641 GCTTGGAGCGTGTCTGGGGTCCTGATTCTAGAGATTGGAT 680
25 681 TAGATACAACCAGTTCAGGAGAGAATTGACCCTCACAGTT 720
721 TTGGACATTGTGTCTCTCTTCCCGAACTATGACTCCAGAA 760
30 761 CCTACCCTATCCGTACAGTGTCCCAACTTACCAGAGAAAT 800

	801	CTATACTAACCCAGTTCTT	840
5	841	CGTGGTTCTGCCCCAAGGTATCGAAGGCTCCATCAGGAGCC	880
	881	CACACTTGATGGACATCTTGAACAGCATAACTATCTACAC	920
	921	CGATGCTCACAGAGGAGAGTATTACTGGTCTGGACACCAG	960
10	961	ATCATGGCCTCTCCAGTTGGATTGAGCGGGCCCGAGTTTA	1000
	1001	CCTTTCCTCTCTATGGAACATATGGGAAACGCCGCTCCACA	1040
15	1041	ACAACGTATCGTTGCTCAACTAGGTCAGGGTGTCTACAGA	1080
	1081	ACCTTGTCTTCCACCTTGTACAGAAGACCCTTCAATATCG	1120
	1121	GTATCAACAACCAGCAACTTCCGTTCTTGACGGAACAGA	1160
20	1161	GTTTCGCCTATGGAACCTCTTCTAACTTGCCATCCGCTGTT	1200
	1201	TACAGAAAGAGCGGAACCGTTGATTCCCTTGGACGAAATCC	1240
	1241	CACCACAGAACAACAATGTGCCACCCAGGCAAGGATTCTC	1280
25	1281	CCACAGGTTGAGCCACGTGTCCATGTTCCGTTCCGGATTG	1320
	1321	AGCAACAGTTCCGTGAGCATCATCAGAGCTCCTATGTTCT	1360
30	1361	CTTGGATACACCGTAGTGCTGAGTTCAACAACATCATCGC	1400

	1401	ATCCGATAGTATTACTCAAATCCCTGCAGTGAAGGGAAAC	1440
5	1441	TTTCTCTTCAACGGTTCTGTCAATTCAGGACCAGGATTCA	1480
	1481	CTGGTGGAGACCTCGTTAGACTCAACAGCAGTGGAAATAA	1520
	1521	CATTCAGAATAGAGGGTATATTGAAGTTCCAATTCACTTC	1560
10	1561	CCATCCACATCTACCAGATATAGAGTTCGTGTGAGGTATG	1600
	1601	CTTCTGTGACCCCTATTCACTCAACGTTAATTGGGGTAA	1640
15	1641	TTCATCCATCTTCTCCAATACAGTTCCAGCTACAGCTACC	1680
	1681	TCCTTGGATAATCTCCAATCCAGCGATTTCGGTTACTTTG	1720
	1721	AAAGTGCCAATGCTTTTACATCTTCACTCGGTAACATCGT	1760
20	1761	GGGTGTTAGAACTTTAGTGGGACTGCAGGAGTGATTATC	1800
	1801	GACAGATTCGAGTTCATTCCAGTTACTGCAACACTCGAGG	1840
	1841	CTGAATATAATCTGGAAAGAGCGCAGAAGGCGGTAATGCG	1880
25	1881	CTGTTTACGTCTACAAACCAGCTTGGACTCAAGACAAATG	1920.

19. A structural gene of Claim 13 encoding the full-length insecticidal protein of *B.t.k.* HD-73 having the sequence:

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1	ATGGACAACAACCCAAACATCAACGAATGCATTCCATACA	40
41	ACTGCTTGAGTAACCCAGAAGTTGAAGTACTTGGTGGAGA	80
81	ACGCATTGAAACCGGTTAACTCCCATCGACATCTCCTTG	120
121	TCCTTGACACAGTTTCTGCTCAGCGAGTTCGTGCCAGGTG	160
161	CTGGGTTTCGTTCTCGGACTAGTTGACATCATCTGGGGTAT	200
201	CTTTGGTCCATCTCAATGGGATGCATTCTTGGTGCAAATT	240
241	GAGCAGTTGATCAACCAGAGGATCGAAGAGTTCGCCAGGA	280
281	ACCAGGCCATCTCTAGGTTGGAAGGATTGAGCAATCTCTA	320
321	CCAAATCTATGCAGAGAGCTTCAGAGAGTGGGAAGCCGAT	360
361	CCTACTAACCCAGCTCTCCGCGAGGAAATGCGTATTCAAT	400
401	TCAACGACATGAACAGGCGCTTGACCACAGCTATCCCATT	440
441	GTTTCGCAGTCCAGAACTACCAAGTTCCTCTCTTGTCCGTG	480
481	TACGTTCAAGCAGCTAATCTTCACCTCAGCGTGCTTCGAG	520
521	ACGTTAGCGTGTTTGGGCAAAGGTGGGGATTTCGATGCTGC	560
561	AACCATCAATAGCCGTTACAACGACCTTACTAGGCTGATT	600

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601 GGAAACTACACCGACCACGCTGTTCGTTGGTACAACACTG 640
641 GCTTGGAGCGTGTCTGGGGTCCTGATTCTAGAGATTGGAT 680
681 TAGATACAACCAGTTCAGGAGAGAATTGACCCTCACAGTT 720
721 TTGGACATTGTGTCTCTCTTCCCGAACTATGACTCCAGAA 760
10
761 CCTACCCTATCCGTACAGTGTCCCAACTTACCAGAGAAAT 800
801 CTATACTAACCCAGTTCTTGAGAACTTCGACGGTAGCTTC 840
15
841 CGTGGTTCTGCCCCAAGGTATCGAAGGCTCCATCAGGAGCC 880
881 CACACTTGATGGACATCTTGAACAGCATAACTATCTACAC 920
921 CGATGCTCACAGAGGAGAGTATTACTGGTCTGGACACCAG 960
20
961 ATCATGGCCTCTCCAGTTGGATTGAGCGGGCCCGAGTTTA 1000
1001 CCTTTCCTCTCTATGGAACATGGGAAACGCCGCTCCACA 1040
1041 ACAACGTATCGTTGCTCAACTAGGTCAGGGTGTCTACAGA 1080
25
1081 ACCTTGTCTTCCACCTTGACAGAAGACCCTTCAATATCG 1120
1121 GTATCAACAACCAGCAACTTCCGTTCTTGACGGAACAGA 1160
30
1161 GTTCGCCTATGGAACCTCTTCTAACTTGCCATCCGCTGTT 1200

1
1201 TACAGAAAGAGCGGAACCGTTGATTCTTGGACGAAATCC 1240
5 1241 CACCACAGAACAACAATGTGCCACCCAGGCAAGGATTCTC 1280
1281 CCACAGGTTGAGCCACGTGTCCATGTTCCGTTCCGGATTTC 1320
1321 AGCAACAGTTCCGTGAGCATCATCAGAGCTCCTATGTTCT 1360
10 1361 CTTGGATACACCGTAGTGCTGAGTTCAACAACATCATCGC 1400
1401 ATCCGATAGTATTACTCAAATCCCTGCAGTGAAGGGAAAC 1440
15 1441 TTTCTCTTCAACGGTTCTGTCAATTCAGGACCAGGATTCA 1480
1481 CTGGTGGAGACCTCGTTAGACTCAACAGCAGTGGAAATAA 1520
1521 CATTCAGAATAGAGGGTATATTGAAGTTCCAATTCCTTC 1560
20 1561 CCATCCACATCTACCAGATATAGAGTTCGTGTGAGGTATG 1600
1601 CTTCTGTGACCCCTATTACCTCAACGTTAATTGGGGTAA 1640
1641 TTCATCCATCTTCTCCAATACAGTTCCAGCTACAGCTACC 1680
25 1681 TCCTTGGATAATCTCCAATCCAGCGATTTTCGGTTACTTTG 1720
1721 AAAGTGCCAATGCTTTTACATCTTCACTCGGTAACATCGT 1760
30 1761 GGGTGTAGAACTTTAGTGGGACTGCAGGAGTGATTATC 1800

	1801	GACAGATTTCGAGTTCATTCCAGTTACTGCAACACTCGAGG	1840
5	1841	CTGAATATAATCTGGAAAGAGCGCAGAAGGCGGTGAATGC	1880
	1881	GCTGTTTACGTCTACAAACCAGCTCGGCCTCAAGACCAAT	1920
	1921	GTGACGGATTATCATATTGATCAAGTGTCCAACCTGGTGA	1960
10	1961	CCTACCTCAGCGATGAGTTCTGTCTGGATGAAAAGCGAGA	2000
	2001	ATTGTCCGAGAAAGTCAAACATGCGAAGCGACTCAGTGAT	2040
15	2041	GAACGCAATTTACTCCAAGATTCAAATTTCAAAGACATTA	2080
	2081	ATAGGCAACCAGAACGTGGGTGGGGCGGAAGTACAGGGAT	2120
	2121	TACCATCCAGGGAGGTGACGACGTGTTCAAGGAGAACTAC	2160
20	2161	GTCACACTATCAGGTACCTTTGATGAGTGCTATCCAACAT	2200
	2201	ACCTCTACCAGAAGATCGACGAGTCCAAGTTGAAAGCCTT	2240
	2241	TACCCGTTATCAATTAAGAGGGTATATCGAAGATAGTCAA	2280
25	2281	GACCTCGAGATCTACCTCATCCGCTACAATGCAAAACATG	2320
	2321	AAACAGTAAATGTGCCAGGTACGGGTTCTTATGGCCGCT	2360
30	2361	TTCAGCCCAAAGTCCAATCGGAAAGTGTGGAGAGCCGAAT	2400

	2401	CGATGCGCGCCACACCTTGAATGGAATCCTGACTTAGATT	2440
5	2441	GTCGTGTAGGGATGGAGAAAAGTGTGCCCATCATTTCGCA	2480
	2481	TCATTTCTCCTTAGACATTGATGTAGGATGTACAGACTTA	2520
	2521	AATGAGGACCTAGGTGTATGGGTGATCTTTAAGATTAAGA	2560
10	2561	CGCAAGATGGGCACGCAAGACTAGGGAATCTAGAGTTTCT	2600
	2601	CGAAGAGAAACCATTAGTAGGAGAAGCGCTAGCTCGTGTG	2640
15	2641	AAAAGAGCGGAGAAAAATGGAGAGACAAACGTGAGAAGT	2680
	2681	TGGAATGGGAGACCAACATCGTCTACAAAGAGGCAAAAGA	2720
	2721	ATCTGTAGATGCTTTATTTGTAAACTCTCAATATGATCAA	2760
20	2761	TTACAAGCGGATACGAATATTGCCATGATTCATGCGGCAG	2800
	2801	ATAAACGTGTTTCATAGCATTTCGAGAAGCTTATCTGCCTGA	2840
25	2841	GCTGTCTGTGATTCCGGGTGTCAATGCGGCTATTTTGTAA	2880
	2881	GAATTAGAAGGGCGTATTTTCACTGCATTCTCCCTCTACG	2920
	2921	ATGCCAGAAACGTCATCAAGAACGGTGAAGTCAACAATGG	2960
30	2961	CTTATCCTGCTGGAACGTGAAAGGGCATGTAGATGTAGAA	3000

5 3001 GAACAAAACAACCAACGTTTCGGTCCTTGTTGTTCCGGAAT 3040
3041 GGAAGCAGAAGTGTACAAGAAGTTCGTGTCTGTCCGGG 3080
3081 TCGTGGCTATATCCTTCGTGTACAGCGTACAAGGAGGGA 3120
10 3121 TATGGAGAAGGTTGCGTAACCATTTCATGAGATCGAGAACA 3160
3161 ATACAGACGAACTGAAGTTTAGCAACTGCGTAGAAGAGGA 3200
3201 AATCTATCCAAATAACACGGTAACGTGTAATGATTATACT 3240
15 3241 GTAAATCAAGAAGAATACGGAGGTGCGTACACTTCTCGTA 3280
3281 ATCGAGGATATAACGAAGCTCCTTCCGTACCAGCTGATTA 3320
3321 TCGGTCAGTCTATGAAGAAAAATCGTATACAGATGGACGA 3360
20 3361 AGAGAGAATCCTTGTTGAATTTAACAGAGGGTATAGGGATT 3400
3401 ACACGCCACTACCAGTTGGTTATGTGACAAAAGAATTAGA 3440
25 3441 ATACTTCCCAGAAACCGATAAGGTATGGATTGAGATTGGA 3480
3481 GAAACGGAAGGAACATTTATCGTGGACAGCGTGGAATTAC 3520
30 3521 TCCTTATGGAGGAA 3534.

20. A structural gene of Claim 13 encoding a full-length insecticidal protein of *B.t.k.* HD-73 having the sequence:

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1 ATGGACAACAACCCAAACATCAACGAATGCATTCCATACA 40
41 ACTGCTTGAGTAACCCAGAAGTTGAAGTACTTGGTGGAGA 80
81 ACGCATTGAAACCGGTTACACTCCCATCGACATCTCCTTG 120
121 TCCTTGACACAGTTTCTGCTCAGCGAGTTCGTGCCAGGTG 160
161 CTGGGTTCGTTCTCGGACTAGTTGACATCATCTGGGGTAT 200
201 CTTTGGTCCATCTCAATGGGATGCATTCCTGGTGCAAATT 240
241 GAGCAGTTGATCAACCAGAGGATCGAAGAGTTCGCCAGGA 280
281 ACCAGGCCATCTCTAGGTTGGAAGGATTGAGCAATCTCTA 320
321 CCAAATCTATGCAGAGAGCTTCAGAGAGTGGGAAGCCGAT 360
361 CCTACTAACCCAGCTCTCCGCGAGGAAATGCGTATTCAAT 400
401 TCAACGACATGAACAGCGCCTTGACCACAGCTATCCCATT 440
441 GTTCGCAGTCCAGAACTACCAAGTTCCTCTCTTGTCCGTG 480
481 TACGTTCAAGCAGCTAATCTTCACCTCAGCGTGCTTCGAG 520

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521	ACGTTAGCGTGTTTGGGCAAAGGTGGGGATTTCGATGCTGC	560
561	AACCATCAATAGCCGTTACAACGACCTTACTAGGCTGATT	600
601	GGAAACTACACCGACCACGCTGTTCGTTGGTACAACACTG	640
641	GCTTGGAGCGTGTCTGGGGTCCTGATTCTAGAGATTGGAT	680
681	TAGATACAACCAGTTCAGGAGAGAATTGACCCTCACAGTT	720
721	TTGGACATTGTGTCTCTCTTCCCGAACTATGACTCCAGAA	760
761	CCTACCCTATCCGTACAGTGTCCCAACTTACCAGAGAAAT	800
801	CTATACTAACCCAGTTCCTTGAGAACTTCGACGGTAGCTTC	840
841	CGTGGTTCTGCCCAAGGTATCGAAGGCTCCATCAGGAGCC	880
881	CACACTTGATGGACATCTTGAACAGCATAACTATCTACAC	920
921	CGATGCTCACAGAGGAGAGTATTACTGGTCTGGACACCAG	960
961	ATCATGGCCTCTCCAGTTGGATTTCAGCGGGCCCGAGTTTA	1000
1001	CCTTTCCTCTCTATGGAAGTATGGGAAACGCCGCTCCACA	1040
1041	ACAACGTATCGTTGCTCAACTAGGTCAGGGTGTCTACAGA	1080
1081	ACCTTGTCTTCCACCTTGTACAGAAGACCCTTCAATATCG	1120

	1121	GTATCAACAACCAGCAACTTTCCGTTCTTGACGGAACAGA	1160
5	1161	GTTCGCCTATGGAACCTCTTCTAACTTGCCATCCGCTGTT	1200
	1201	TACAGAAAGAGCGGAACCGTTGATTCCTTGGACGAAATCC	1240
	1241	CACCACAGAACAACAATGTGCCACCCAGGCAAGGATTCTC	1280
10	1281	CCACAGGTTGAGCCACGTGTCCATGTTCCGTTCCGGATTCT	1320
	1321	AGCAACAGTTCCGTGAGCATCATCAGAGCTCCTATGTTCT	1360
15	1361	CTTGGATACACCGTAGTGCTGAGTTCAACAACATCATCGC	1400
	1401	ATCCGATAGTATTACTCAAATCCCTGCAGTGAAGGGAAAC	1440
	1441	TTTCTCTTCAACGGTTCTGTCAATTCAGGACCAGGATTCA	1480
20	1481	CTGGTGGAGACCTCGTTAGACTCAACAGCAGTGGAAATAA	1520
	1521	CATTCAGAATAGAGGGTATATTGAAGTTCCAATTCACTTC	1560
25	1561	CCATCCACATCTACCAGATATAGAGTTCGTGTGAGGTATG	1600
	1601	CTTCTGTGACCCCTATTACCTCAACGTTAATTGGGGTAA	1640
	1641	TTCATCCATCTTCTCCAATACAGTTCCAGCTACAGCTACC	1680
30	1681	TCCTTGGATAATCTCCAATCCAGCGATTTCGGTTACTTTG	1720

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1721 AAAGTGCCAATGCTTTTACATCTTCACTCGGTAACATCGT 1760
1761 GGGTGTTAGAACTTTAGTGGGACTGCAGGAGTGATTATC 1800
1801 GACAGATTCGAGTTCATTCCAGTTACTGCAACACTCGAGG 1840
1841 CTGAATATAATCTGGAAAGAGCGCAGAAGGCGGTGAATGC 1880
1881 GCTGTTTACGTCTACAAACCACTAGGGCTAAAAACAAT 1920
1921 GTAACGGATTATCATATTGATCAAGTGTCCAATTTAGTTA 1960
1961 CGTATTTATCGGATGAATTTTGTCTGGATGAAAAGCGAGA 2000
2001 ATTGTCCGAGAAAGTCAAACATGCGAAGCGACTCAGTGAT 2040
2041 GAACGCAATTTACTCCAAGATTCAAATTTCAAAGACATTA 2080
2081 ATAGGCAACCAGAACGTGGGTGGGGCGGAAGTACAGGGAT 2120
2121 TACCATCCAAGGAGGGGATGACGTATTTAAAGAAAATTAC 2160
2161 GTCACACTATCAGGTACCTTTGATGAGTGCTATCCAACAT 2200
2201 ATTTGTATCAAAAAATCGATGAATCAAATTTAAAGCCTT 2240
2241 TACCCGTTATCAATTAAGAGGGTATATCGAAGATAGTCAA 2280
2281 GACTTAGAAATCTATTTAATTCGCTACAATGCAAAACATG 2320

2321 AAACAGTAAATGTGCCAGGTACGGGTTCCTTATGGCCGCT 2360
5 2361 TTCAGCCCAAAGTCCAATCGGAAAGTGTGGAGAGCCGAAT 2400
2401 CGATGCGCGCCACACCTTGAATGGAATCCTGACTTAGATT 2440
2441 GTTCGTGTAGGGATGGAGAAAAGTGTGCCCATCATTCGCA 2480
10 2481 TCATTTCTCCTTAGACATTGATGTAGGATGTACAGACTTA 2520
2521 AATGAGGACCTAGGTGTATGGGTGATCTTTAAGATTAAGA 2560
15 2561 CGCAAGATGGGCACGCAAGACTAGGGAATCTAGAGTTTCT 2600
2601 CGAAGAGAAACCATTAGTAGGAGAAGCGCTAGCTCGTGTG 2640
2641 AAAAGAGCGGAGAAAAAATGGAGAGACAAACGTGAAAAAT 2680
20 2681 TGGAATGGGAAACAAATATCGTTTATAAAGAGGCAAAGA 2720
2721 ATCTGTAGATGCTTTATTTGTAAACTCTCAATATGATCAA 2760
2761 TTACAAGCGGATACGAATATTGCCATGATTCATGCGGCAG 2800
25 2801 ATAAACGTGTTTCATAGCATTGAGAGAAGCTTATCTGCCTGA 2840
2841 GCTGTCTGTGATTCCGGGTGTCAATGCGGCTATTTTGA 2880
30 2881 GAATTAGAAGGGCGTATTTTCACTGCATTCTCCCTATATG 2920

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2921	ATGCGAGAAATGTCATTAAAAATGGTGATTTTAATAATGG	2960
2961	CTTATCCTGCTGGAACGTGAAAGGGCATGTAGATGTAGAA	3000
3001	GAACAAAACAACCAACGTTCCGGTCCTTGTTGTTCCGGAAT	3040
3041	GGGAAGCAGAAGTGTACACAAGAAGTTCGTGTCTGTCCGGG	3080
3081	TCGTGGCTATATCCTTCGTGTACAGCGTACAAGGAGGGA	3120
3121	TATGGAGAAGGTTGCGTAACCATTGAGATCGAGAACA	3160
3161	ATACAGACGAACTGAAGTTTAGCAACTGCGTAGAAGAGGA	3200
3201	AATCTATCCAAATAACACGGTAACGTGTAATGATTATACT	3240
3241	GTAAATCAAGAAGAATACGGAGGTGCGTACACTTCTCGTA	3280
3281	ATCGAGGATATAACGAAGCTCCTTCCGTACCAGCTGATTA	3320
3321	TGCGTCAGTCTATGAAGAAAATCGTATACAGATGGACGA	3360
3361	AGAGAGAATCCTTGTGAATTTAACAGAGGGTATAGGGATT	3400
3401	ACACGCCACTACCAGTTGGTTATGTGACAAAAGAATTAGA	3440
3441	ATACTTCCCAGAAACCGATAAGGTATGGATTGAGATTGGA	3480

3481 GAAACGGAAGGAACATTTATCGTGGACAGCGTGGAATTAC 3520

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3521 TCCTTATGGAGGAA 3534.

21. A structural gene of Claim 13 encoding a full-length insecticidal protein of *B.t.k.* HD-73 having the sequence:

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1 ATGGACAACAACCCAAACATCAACGAATGCATTCCATACA 40

41 ACTGCTTGAGTAACCCAGAAGTTGAAGTACTGGTGGAGA 80

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81 ACGCATTGAAACCGGTTACTCTCCATCGACATCTCCTTG 120

121 TCCTTGACACAGTTTCTGCTCAGCGAGTTCGTGCCAGGTG 160

161 CTGGGTTCGTTCTCGGACTAGTTGACATCATCTGGGGTAT 200

20

201 CTTTGGTCCATCTCAATGGGATGCATTCCCTGGTGCAAATT 240

241 GAGCAGTTGATCAACCAGAGGATCGAAGAGTTCGCCAGGA 280

25

281 ACCAGGCCATCTCTAGGTTGGAAGGATTGAGCAATCTCTA 320

321 CCAAATCTATGCAGAGAGCTTCAGAGAGTGGGAAGCCGAT 360

361 CCTACTAACCCAGCTCTCCGCGAGGAAATGCGTATTCAAT 400

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401 TCAACGACATGAACAGCGCCTTGACCACAGCTATCCCATT 440

441 GTTCGCAGTCCAGAACTACCAAGTTCCTCTCTTGTCCGTG 480
5 481 TACGTTCAAGCAGCTAATCTTCACCTCAGCGTGCTTCGAG 520
521 ACGTTAGCGTGTTTGGGCAAAGGTGGGGATTTCGATGCTGC 560
561 AACCATCAATAGCCGTTACAACGACCTTACTAGGCTGATT 600
10 601 GGAAACTACACCGACCACGCTGTTCGTTGGTACAACACTG 640
641 GCTTGGAGCGTGTCTGGGGTCCTGATTCTAGAGATTGGAT 680
15 681 TAGATACAACCAGTTCAGGAGAGAATTGACCCTCACAGTT 720
721 TTGGACATTGTGTCTCTCTTCCCGAACTATGACTCCAGAA 760
761 CCTACCCTATCCGTACAGTGTCCCAACTTACCAGAGAAAT 800
20 801 CTATACTAACCCAGTTCTTGAGAACTTCGACGGTAGCTTC 840
841 CGTGGTTCTGCCCCAAGGTATCGAAGGCTCCATCAGGAGCC 880
25 881 CAACTTGATGGACATCTTGAACAGCATAACTATCTACAC 920
921 CGATGCTCACAGAGGAGAGTATTACTGGTCTGGACACCAG 960
961 ATCATGGCCTCTCCAGTTGGATTTCAGCGGGCCCGAGTTTA 1000
30 1001 CCTTTCCTCTCTATGGAACCTATGGGAAACGCCGCTCCACA 1040

1041 ACAACGTATCGTTGCTCAACTAGGTCAGGGTGTCTACAGA 1080
5 1081 ACCTTGTCTTCCACCTGTACAGAAGACCCTTCAATATCG 1120
1121 GTATCAACAACCAGCAACTTCCGTTCTTGACGGAACAGA 1160
1161 GTTCGCCTATGGAACCTCTTCTAACTTGCCATCCGCTGTT 1200
10 1201 TACAGAAAGAGCGGAACCGTTGATTCTTGACGAAATCC 1240
1241 CACCACAGAACAACAATGTGCCACCCAGGCAAGGATTCTC 1280
15 1281 CCACAGGTTGAGCCACGTGTCCATGTTCCGTTCCGGATTC 1320
1321 AGCAACAGTTCCGTGAGCATCATCAGAGCTCCTATGTTCT 1360
1361 CTTGGATACACCGTAGTGCTGAGTTCAACAACATCATCGC 1400
20 1401 ATCCGATAGTATTACTCAAATCCCTGCAGTGAAGGGAAAC 1440
1441 TTTCTCTTCAACGGTTCTGTCAATTCAGGACCAGGATTCA 1480
1481 CTGGTGGAGACCTCGTTAGACTCAACAGCAGTGGAAATAA 1520
25 1521 CATTTCAGAAATAGAGGGTATATTGAAGTTCCAATTCATTC 1560
1561 CCATCCACATCTACCAGATATAGAGTTCGTGTGAGGTATG 1600
30 1601 CTTCTGTGACCCCTATTCACTCAACGTTAATTGGGGTAA 1640

	1641	TTCATCCATCTTCTCCAATACAGTTCCAGCTACAGCTACC	1680
5	1681	TCCTTGGATAATCTCCAATCCAGCGATTTCGGTTACTTTG	1720
	1721	AAAGTGCCAATGCTTTTACATCTTCACTCGGTAACATCGT	1760
	1761	GGGTGTTAGAACTTTAGTGGGACTGCAGGAGTGATTATC	1800
10	1801	GACAGATTCGAGTTCATTCCAGTTACTGCAACACTCGAGG	1840
	1841	CTGAGTACAACCTTGAGAGAGCCCAGAAGGCTGTGAACGC	1880
15	1881	CCTCTTTACCTCCACCAATCAGCTTGGCTTGAAAATAAC	1920
	1921	GTTACTGACTATCACATTGACCAAGTGCCAAGTGGTCA	1960
	1961	CCTACCTTAGCGATGAGTTCTGCCTCGACGAGAAGCGTGA	2000
20	2001	ACTCTCCGAGAAAGTTAAACACGCCAAGCGTCTCAGCGAC	2040
	2041	GAGAGGAATCTCTTGCAAGACTCCAAGTCAAAGACATCA	2080
25	2081	ACAGGCAGCCAGAACGTGGTTGGGGTGGAAGCACCAGGAT	2120
	2121	CACCATCCAAGGAGGCGACGATGTGTTCAAGGAGAACTAC	2160
	2161	GTCACCCTCTCCGGAACCTTCGACGAGTGCTACCCTACCT	2200
30	2201	ACTTGTACCAGAAGATCGATGAGTCCAACTCAAAGCCTT	2240

2241 CACCAGGTATCAACTTAGAGGCTACATCGAAGACAGCCAA 2280
5 2281 GACCTTGAAATCTACTCGATCAGGTACAATGCCAAGCACG 2320
2321 AGACCGTGAATGTCCCAGGTACTGGTTCCTCTGGCCACT 2360
2361 TTCTGCCCAATCTCCCATTGGGAAGTGTGGAGAGCCTAAC 2400
10 2401 AGATGCGCTCCACACCTTGAGTGGAATCCTGACTTGGACT 2440
2441 GCTCCTGCAGGGATGGCGAGAAGTGTGCCACCATTCTCA 2480
15 2481 TCACTTCTCCTTGGACATCGATGTGGGATGTACTGACCTG 2520
2521 AATGAGGACCTCGGAGTCTGGGTCATCTTCAAGATCAAGA 2560
2561 CCCAAGACGGACACGCAAGACTTGGCAACCTTGAGTTTCT 2600
20 2601 CGAAGAGAAACCATTGGTCGGTGAAGCTCTCGCTCGTGTG 2640
2641 AAGAGAGCAGAGAAGAAGTGGAGGGACAAACGTGAGAAAC 2680
2681 TCGAATGGGAAACTAACATCGTTTACAAGGAGGCCAAAGA 2720
25 2721 GTCCGTGGATGCTTTGTTCTGTAACCTCCAATATGATCAG 2760
2761 TTGCAAGCCGACACCAACATCGCCATGATCCACGCCGCAG 2800
30 2801 ACAAACGTGTGCACAGCATTTCGTGAGGCTTACTTGCCTGA 2840

	2841	GTTGTCCGTGATCCCTGGTGTGAACGCTGCCATCTTCGAG	2880
5	2881	GAACCTGAGGGACGTATCTTTACCGCATTCTCCTTGTACG	2920
	2921	ATGCCAGAAACGTCATCAAGAACGGTGAAGGTCATGTGGACGTGGAG	2960
	2961	CCTCAGCTGCTGGAATGTGAAAGGTCATGTGGACGTGGAG	3000
10	3001	GAACAGAACAATCAGCGTTCCGTCCTGGTTGTGCCTGAGT	3040
	3041	GGGAAGCTGAAGTGTCCCAAGAGGTTAGAGTCTGTCCAGG	3080
15	3081	TAGAGGCTACATTCTCCGTGTGACCGCTTACAAGGAGGGA	3120
	3121	TACGGTGAGGGTTGCGTGACCATCCACGAGATCGAGAACA	3160
	3161	ACACCGACGAGCTTAAGTTCTCCAAGTGCCTCGAGGAAGA	3200
20	3201	AATCTATCCCAACAACACCGTTACTTGCAACGACTACACT	3240
	3241	GTGAATCAGGAAGAGTACGGAGGTGCCTACACTAGCCGTA	3280
25	3281	ACAGAGGTTACAACGAAGCTCCTTCCGTTCTGCTGACTA	3320
	3321	TGCCTCCGTGTACGAGGAGAAATCCTACACAGATGGCAGA	3360
	3361	CGTGAGAACCCTTGCGAGTTCAACAGAGGTTACAGGGACT	3400
30	3401	ACACACCACTTCCAGTTGGCTATGTTACCAAGGAGCTTGA	3440

3441 GTACTTTCCTGAGACCGACAAAGTGTGGATCGAGATCGGT 3480
 5 3481 GAAACCGAGGGAACCTTCATCGTGGACAGCGTGGAGCTTC 3520
 3521 TCTTGATGGAGGAA 3534.

22. A structural gene of Claim 13 which encodes an
 10 insecticidal protein of *B.t.t.* having the sequence:

1 ATGACTGCAGACAACAACACCGAAGCCCTCGACAGTTCTA 40
 41 CCACTAAGGATGTTATCCAGAAGGGTATCTCCGTTGTGGG 80
 15 81 AGACCTCTTGGGCGTGGTTGGATTTCCTTCGGTGGAGCC 120
 121 CTCGTGAGCTTCTATACAACTTTCTCAACACCATTGTC 160
 20 161 CAAGCGAGGACCCTTGAAAGCATTTCATGGAGCAAGTTGA 200
 201 AGCTCTTATGGATCAGAAGATTGCAGATTATGCCAAGAAC 240
 241 AAGGCTTTGGCAGAACTCCAGGGCCTTCAGAACAAATGTGG 280
 25 281 AGGACTACGTGAGTGCATTGTCCAGCTGGCAGAAGAACCC 320
 321 TGTTAGCTCCAGAAATCCTCACAGCCAAGGTAGGATCAGA 360
 361 GAGTTGTTCTCTCAAGCCGAATCCCACTTCAGAAATTCCA 400

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401 TGCCTAGCTTTGCTATCTCCGGTTACGAGGTTCTTTTCCT 440
441 CACTACCTATGCTCAAGCTGCCAACACCCACTTGTTTCTC 480
481 CTTAAGGACGCTCAAATCTATGGAGAAGAGTGGGGATACG 520
521 AGAAAGAGGACATTGCTGAGTTCTACAAGCGTCAACTTAA 560
561 GCTCACCCAAGAGTACACTGACCATTGCGTGAAATGGTAT 600
601 AACGTTGGTCTCGATAAGCTCAGAGGCTCTTCCTACGAGT 640
641 CTTGGGTGAACTTCAACAGATACAGGAGAGAGATGACCTT 680
681 GACTGTGCTCGATCTTATCGCACTCTTTCCCTTGACGAT 720
721 GTGAGACTCTACCCAAAGGAAGTGAAAAGTGAAGCTTACCA 760
761 GAGACGTGCTCACTGACCCCTATTGTCGGAGTCAACAACCT 800
801 TAGGGGTTATGGAACTACCTTCAGCAATATCGAAAAGTAC 840
841 ATTAGGAAACCACATCTCTTCGACTATCTTCACAGAATTC 880
881 AATTCCACACAAGGTTTCAACCAGGATACTATGGTAACGA 920
921 CTCCTTCAACTATTGGTCCGGTAACTATGTTTCCACCAGA 960
961 CCAAGCATTGGATCTAATGACATCATCACATCTCCCTTCT 1000

	1001	ATGGTAACAAGTCCAGTGAACCTGTGCAGAACCTTGAGTT	1040
5	1041	CAACGGCGAGAAAGTCTATAGAGCCGTCGCAAACACCAAT	1080
	1081	CTCGCTGTGTGGCCATCCGCAGTTTACTCAGGCGTCACAA	1120
	1121	AGGTGGAGTTTAGTCAGTATAACGATCAGACCGATGAGGC	1160
10	1161	CAGCACCCAGACTTACGACTCCAAACGTAACGTTGGCGCA	1200
	1201	GTCTCTTGGGATTCTATCGACCAATTGCCTCCAGAAACCA	1240
15	1241	CAGACGAACCATTGGAGAAGGGCTACAGCCACCAACTTAA	1280
	1281	CTATGTGATGTGCTTCTTGATGCAAGGTTCCAGAGGGACC	1320
	1321	ATTCCAGTGTTGACCTGGACACACAAGTCCGTGGACTTCT	1360
20	1361	TCAACATGATCGATAGCAAGAAGATCACTCAACTTCCCTT	1400
	1401	GGTGAAAGCCTACAAGCTGCAATCTGGTGCTTCCGTTGTC	1440
	1441	GCAGGTCCCAGATTCACTGGAGGTGACATCATCCAGTGCA	1480
25	1481	CAGAGAACGGCAGCGCAGCTACTATCTACGTGACACCTGA	1520
	1521	TGTGTCTTACTCTCAGAAGTACAGGGCACGTATTCATTAC	1560
30	1561	GCATCTACCAGCCAGATCACCTTCACACTCAGCTTGGATG	1600

1601 GAGCACCTTCAACCAGTATTACTTTGACAAGACCATCAA 1640
5 1641 CAAAGGTGACACTCTCACATACAATAGCTTCAACTTGGCA 1680
1681 AGTTTCAGCACACCATTGTGAAGTCTCAGGCAACAATCTTC 1720
1721 AGATCGGCGTCACCGGTCTCAGCGCCGGAGACAAAGTCTA 1760
10 1761 CATCGACAAGATTGAGTTGATCCCAAGTGAAC 1791.

23. A structural gene of Claim 13 which encodes an
insecticidal protein of *B.t. entomocidus* having the
15 sequence:

1 ATGGAGGAGAACAACCAAAACCAATGCATTCCATACAAC 40
41 GCTTGAGTAACCCAGAAGAGGTATTGCTTGATGGAGAACG 80
20 81 CATTTCAACCGGTAAGTCTTCCATCGACATCTCCTTGTC 120
121 TTGGTCCAGTTTCTGGTCAGCAACTTCGTGCCAGGTGGTG 160
161 GGTTCTTGTCGGACTAATTGACTTCGTCTGGGGTATCGT 200
25 201 TGGTCCATCTCAATGGGATGCAATTCCTGGTGCAAATTGAG 240
241 CAGTTGATCAACGAGAGGATCGCTGAGTTCGCCAGGAACG 280
30 281 CTGCCATCGCTAACTTGAAGGATTGGGCAATAACTTCAA 320

321 CATCTATGTGGAGGCCTTCAAAGAGTGGGAAGAGGACCCT 360
5 361 AACAAACCAGAGACCCGCACTAGGGTGATCGACAGATTCA 400
401 GAATCTTGGACGGCCTCTTGGAGAGAGATATCCCATCCTT 440
441 CAGAATCTCTGGCTTCGAAGTTCCTCTCTTGTCCGTGTAC 480
10 481 GCTCAAGCAGCTAATCTTCACTCGCTATCCTTCGAGACA 520
521 GTGTCATCTTTGGGGAAAGGTGGGGATTGACCACTATCAA 560
15 561 CGTCAATGAGAATTACAACAGACTTATCAGGCACATTGAC 600
601 GAGTACGCCGACCACTGTGCTAACACCTACAACCGTGGCT 640
641 TGAACAATCTCCCTAAGTCTACTTATCAAGATTGGATTAC 680
20 681 CTACAACAGGTTGAGGAGAGACTTGACCCTCACAGTTTTG 720
721 GACATTGCAGCTTTCTTCCCGAACTATGACAACAGGAGAT 760
761 ACCCTATCCAACCAGTGGGTCAACTTACCAGAGAAGTCTA 800
25 801 TACTGACCCACTTATCAACTTCAACCCTCAGTTGCAAAGT 840
841 GTCGCCCAACTTCCCACATTCAACGTCATGGAGTCCAGCC 880
30 881 GTATCAGGAACCCACACTTGTGTTGACATCTTGAACAACCT 920

5 921 TACTATCTTCACCGATTGGTTTCAGCGTTGGGCGTAACTTC 960
5 961 TATTGGGGTGGACACAGGGTCATCTCCTCTCTTATTGGAG 1000
1001 GTGGGAACATTACCTCTCCTATCTATGGACGTGAGGCAA 1040
1041 CCAGGAGCCACCACGTAGTTTCACCTTCAACGGTCCAGTC 1080
10 1081 TTCAGAACCTTGTCTAACCTACCTTGAGATTGCTCCAGC 1120
1121 AACCTTGGCCAGCTCCACCTTTCAACCTTAGAGGTGTTGA 1160
15 1161 GGGCGTTGAGTTCTCTACTCCTACCAACTCCTTCACTTAC 1200
1201 AGAGGTAGAGGAACCGTTGATTCCTTGACCGAACTCCCAC 1240
1241 CAGAGGACAATAGCGTGCCACCCAGGGAAGGCTACTCCCA 1280
20 1281 CAGGTTGTGCCACGCAACCTTCGTGCAGCGTTCCGGAACT 1320
1321 CCATTCTCTACTACAGGAGTTGTGTTCTCATGGACTGATC 1360
1361 GTAGTGCTACTCTCACTAATACCATTGATCCCGAGAGGAT 1400
25 1401 CAATCAAATCCCATTGGTCAAGGGTTCCGTGTGTGGGGA 1440
1441 GGAACCTTCTGTTCATCACAGGACCAGGCTTCACAGGAGGTG 1480
30 1481 ATATTCTTAGAAGAAACACTTTTGGCGACTTTGTGAGCCT 1520

1521 CCAAGTTAACATCAACTCTCCAATTACTCAAAGATATCGT 1560
5 1561 CTCAGGTTTCGTTACGCATCTTCCCGTGACGCTAGAGTCA 1600
1601 TCGTGCTCACCGGAGCAGCTTCTACCGGTGTCGGTGGACA 1640
1641 AGTCTCCGTGAACATGCCACTCCAGAAGACTATGGAGATC 1680
10 1681 GGCGAGAACTTGACATCCAGGACCTTCAGATACACCGACT 1720
1721 TCTCTAACCCTTTCAGTTTCGTGCCAACCCTGACATCAT 1760
15 1761 TGGCATTAGCGAACAACCTCTCTTTGGAGCTGGTAGCATC 1800
1801 TCATCTGGCGAATTGTACATTGACAAGATTGAGATCATTC 1840
1841 TTGCCGACGCTACCTTCGAGGCTGAGTCTGACCTTGAGAG 1880
20 1881 AGCCCAGAAGGCTGTGAACGCCCTCTTTACCTCCTCTAAT 1920
1921 CAGATTGGCTTGAAAAGTACGTTACTGACTATCACATTG 1960
1961 ACCAAGTGTCCAACCTGGTCGACTGCCTTAGCGATGAGTT 2000
25 2001 CTGCCTCGACGAGAAGCGTGAAGTCTCCGAGAAAGTTAAA 2040
2041 CACGCCAAGCGTCTCAGCGACGAGAGGAATCTCTTGCAAG 2080
30 2081 ACCCCAACCTTCAGAGGCATCAACAGGCAGCCAGACCGTGG 2120

	2121	TTGGAGAGGAAGCACCGACATCACCATCCAAGGAGGCGAC	2160
5	2161	GATGTGTTCAAGGAGAACTACGTCACCCTCCCAGGAACTG	2200
	2201	TGGACGAGTGCTACCCTACCTACTTGTACCAGAAGATCGA	2240
	2241	TGAGTCCAAACTCAAAGCCTACACCAGGTATGAACTTAGA	2280
10	2281	GGCTACATCGAAGACAGCCAAGACCTTGAAATCTACCTCA	2320
	2321	TCAGGTACAATGCCAAGCACGAGATCGTGAATGTCCCAGG	2360
15	2361	TACTGGTTCCCTCTGGCCACTTTCTGCCCAAATGCCCAT	2400
	2401	GGGAAGTGTGGAGAGCCTAACAGATGCGCTCCACACCTTG	2440
	2441	AGTGAATCCTGACTTGGAAGTCTCCTGCAGGGATGGCGA	2480
20	2481	GAAGTGTGCCCACCATTCTCATCACTTCACCTTGGACATC	2520
	2521	GATGTGGGATGTACTGACCTGAATGAGGACCTCGGAGTCT	2560
	2561	GGGTCATCTTCAAGATCAAGACCCAAGACGGACACGCAAG	2600
25	2601	ACTTGGCAACCTTGAGTTTCTCGAAGAGAAACCATTGCTC	2640
	2641	GGTGAAGCTCTCGCTCGTGTGAAGAGAGCAGAGAAGAAGT	2680
30	2681	GGAGGGACAAACGTGAGAACTCCAACCTCGAGACTAACAT	2720

2721 CGTTTACAAGGAGGCCAAAGAGTCCGTGGATGCTTTGTTC 2760
5 2761 GTGAACTCCCAATATGATAGCTTGCAAGTGGACACCAACA 2800
2801 TCGCCATGATCCACGCTGCAGACAAACGTGTGCACAGGAT 2840
2841 TCGTGAGGCTTACTTGCCTGAGTTGTCCGTGATCCCTGGT 2880
10 2881 GTGAACGCTGCCATCTTCGAGGAAGTTGAGGGACGTATCT 2920
2921 TTACCGCATACTCCTTGTACGATGCCAGAAACGTCATCAA 2960
15 2961 GAACGGTGACTTCAACAATGCCCTCTTGTGCTGGAATGTG 3000
3001 AAAGGTCATGTGGACGTGGAGGAACAGAACAATCACCGTT 3040
3041 CCGTCCTGGTTATCCCTGAGTGGGAAGCTGAAGTGTCCCA 3080
20 3081 AGAGGTTAGAGTCTGTCCAGGTAGAGGCTACATTCTCCGT 3120
3121 GTGACCGCTTACAAGGAGGGATACGGTGAGGGTTGCGTGA 3160
3161 CCATCCACGAGATCGAGGACAACACCGACGAGCTTAAGTT 3200
25 3201 CTCCAACGCGTCGAGGAAGAAGTCTATCCCAACAACACC 3240
3241 GTTACTTGCAACAACACTACACTGGGACCCAGGAAGAGTACG 3280
30 3281 AAGGTACCTACACTAGCCGTAACCAAGGTTACGACGAAGC 3320

3321 TTACGGAAACAATCCTTCGTTCCCTGCTGACTATGCCTCC 3360
 5 3361 GTGTACGAGGAGAAATCCTACACAGATGGCAGACGTGAGA 3400
 3401 ACCCTTGCGAGTCCAACAGAGGTTACGGTGACTACACACC 3440
 3441 ACTTCCAGCAGGCTATGTTACCAAGGACCTTGAGTACTTT 3480
 10 3481 CCTGAGACCGACAAAGTGTGGATCGAGATCGGTGAAACCG 3520
 3521 AGGGAACCTTCATCGTGGACAGCGTGGAGCTTCTCTTGAT 3560
 15 3561 GGAGGAA 3567.

24. A structural gene of Claim 13 which encodes a P2 insecticidal protein having the sequence:

20 1 ATGGACAACAACGTCTTGA ACTCTGGTAGAACAACCATCT 40
 41 GCGACGCATACAACGTCGTGGCTCACGATCCATT CAGCTT 80
 81 CGAACACAAGAGCCTCGACACTATT CAGAAGGAGTGGATG 120
 25 121 GAATGGAAACGTACTGACCACTCTCTCTACGTCGCACCTG 160
 161 TGGTTGGAACAGTGTCCAGCTTCCTTCTCAAGAAGGTCGG 200
 201 CTCTCTCATCGGAAAACGTATCTTGTCCGAACTCTGGGGT 240
 30

241 ATCATCTTTCCATCTGGGTCCACTAATCTCATGCAAGACA 280
5 281 TCTTGAGGGAGACCGAACAGTTTCTCAACCAGCGTCTCAA 320
321 CACTGATACCTTGGCTAGAGTCAACGCTGAGTTGATCGGT 360
361 CTCCAAGCAAACATTTCGTGAGTTCAACCAGCAAGTGGACA 400
10 401 ACTTCTTGAATCCAACTCAGAATCCTGTGCCTCTTTCCAT 440
441 CACTTCTTCCGTGAACACTATGCAGCAACTCTTCCTCAAC 480
15 481 AGATTGCCTCAGTTTCAGATTCAAGGCTACCAGTTGCTCC 520
521 TTCTTCCACTCTTTGCTCAGGCTGCCAACATGCACTTGTC 560
561 CTTCATACGTGACGTGATGCTCAACGCTGACGAATGGGGA 600
20 601 ATCTCTGCAGCCACTCTTAGGACATACAGAGACTACTTGA 640
641 GGAACTACACTCGTGATTACTCCAACATATTGCATCAACAC 680
681 TTATCAGACTGCCTTTCGTGGACTCAATACTAGGCTTCAC 720
25 721 GACATGCTTGAGTTCAGGACCTACATGTTTCCTTAACGTGT 760
761 TTGAGTACGTGAGCATTGAGTCTCTTCAAGTACCAGAG 800
30 801 CTTGATGGTGTCTCTGGAGCCAATCTCTACGCCTCTGGC 840

5 841 AGTGGACCACAGCAAACCTCAGAGCTTCACAGCTCAGAACT 880
881 GGCCATTCTTGTATAGCTTGTTCCAAGTCAACTCCAATA 920
921 CATTCTCAGTGGTATCTCTGGGACCAGACTCTCCATAACC 960
10 961 TTTCCCAACATTGGTGGACTTCCAGGCTCCACTACAACCC 1000
1001 ATAGCCTTAACTCTGCCAGAGTGAACCTACAGTGGAGGTGT 1040
1041 CAGCTCTGGATTGATTGGTGCAACTAACTTGAACCACAAC 1080
15 1081 TTCAATTGCTCCACCGTCTTGCCACCTCTGAGCACACCGT 1120
1121 TTGTGAGGTCCCTGGCTTGACAGCGGTACTGATCGCGAAGG 1160
1161 AGTTGCTACCTCTACAACTGGCAAACCGAGTCCTTCCAA 1200
20 1201 ACCACTCTTAGCCTTCGGTGTGGAGCTTCTCTGCACGTG 1240
1241 GGAATTCAAACCTACTTTCCAGACTACTTCATTAGGAACAT 1280
1281 CTCTGGTGTTCCTCTCGTCATCAGGAATGAAGACCTCACC 1320
25 1321 CGTCCACTTCATTACAACAGATTAGGAACATCGAGTCTC 1360
1361 CATCCGGTACTCCAGGAGGTGCAAGAGCTTACCTCGTGTC 1400
30 1401 TGTCCATAACAGGAAGAACAACATCTACGCTGCCAACGAG 1440

1441 AATGGCACCATGATTACCTTGCACCAGAAGATTACACTG 1480
 5 1481 GATTCAACCATCTCTCCAATCCATGCTACCCAAGTGAACAA 1520
 1521 TCAGACACGCACCTTCATCTCCGAAAAGTTCGGAAATCAA 1560
 1561 GGTGACTCCTTGAGGTTTCGAGCAATCCAACACTACCGCTA 1600
 10 1601 GGTACACTTTGAGAGGCAATGGAAACAGCTACAACCTTTA 1640
 1641 CTTGAGAGTTAGCTCCATTGGTAACTCCACCATCCGTGTT 1680
 15 1681 ACCATCAACGGACGTGTTTACACAGTCTCTAATGTGAACA 1720
 1721 CTACAACGAACAATGATGGCGTTAACGACAACGGAGCCAG 1760
 1761 ATTCAGCGACATCAACATTGGCAACATCGTGGCCTCTGAC 1800
 20 1801 AACACTAACGTTACTTTGGACATCAATGTGACCCTCAATT 1840
 1841 CTGGAACCTCCATTTGATCTCATGAACATCATGTTTGTGCC 1880
 25 1881 AACTAACCTCCCTCCATTGTACTAA 1905.

25. A plant transformation vector comprising a plant gene containing a structural gene of Claim 13.

26. A structural gene sequence of Claim 13
encoding a fusion protein comprising the N-terminal
610 amino acids of *B.t.k.* HD-1 and the C-terminal 567
amino acids of *B.t.k.* HD-73, said gene having the
sequence:

1 ATGGACAACAACCCAAACATCAACGAATGCATTCCATACA 40
10 41 ACTGCTTGAGTAACCCAGAAGTTGAAGTACTTGGTGGAGA 80
81 ACGCATTGAAACCGGTTACACTCCCATCGACATCTCCTTG 120
121 TCCTTGACACAGTTTCTGCTCAGCGAGTTCGTGCCAGGTG 160
15 161 CTGGGTTCGTTCTCGGACTAGTTGACATCATCTGGGGTAT 200
201 CTTTGGTCCATCTCAATGGGATGCATTCCTGGTGCAAATT 240
241 GAGCAGTTGATCAACCAGAGGATCGAAGAGTTCGCCAGGA 280
20 281 ACCAGGCCATCTCTAGGTGGAAGGATTGAGCAATCTCTA 320
321 CCAAATCTATGCAGAGAGCTTCAGAGAGTGGAAGCCGAT 360
25 361 CCTACTAACCCAGCTCTCCGCGAGGAAATGCGTATTCAAT 400
401 TCAACGACATGAACAGCGCCTTGACCACAGCTATCCCATT 440

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441 GTTCGCAGTCCAGAACTACCAAGTTCCTCTCTTGTCCTG 480

5 481 TACGTTCAAGCAGCTAATCTTCACCTCAGCGTGCTTCGAG 520

521 ACGTTAGCGTGTTTGGGCAAAGGTGGGGATTTCGATGCTGC 560

561 AACCATCAATAGCCGTTACAACGACCTTACTAGGCTGATT 600

10 601 GGAAACTACACCGACCACGCTGTTTCGTTGGTACAACACTG 640

641 GCTTGGAGCGTGTCTGGGGTCTGATTCTAGAGATTGGAT 680

681 TAGATACAACCAGTTCAGGAGAGAATTGACCCTCACAGTT 720

721 TTGGACATTGTGTCTCTCTTCCCGAACTATGACTCCAGAA 760

761 CCTACCCTATCCGTACAGTGTCCCAACTTACCAGAGAAAT 800

20 801 CTATACTAACCCAGTTCTTGAGAACTTCGACGGTAGCTTC 840

841 CGTGGTTCTGCCCCAAGGTATCGAAGGCTCCATCAGGAGCC 880

881 CACACTTGATGGACATCTTGAACAGCATAACTATCTACAC 920

25 921 CGATGCTCACAGAGGAGAGTATTACTGGTCTGGACACCAG 960

961 ATCATGGCCTCTCCAGTTGGATTTCAGCGGGCCCGAGTTTA 1000

30 1001 CCTTCCTCTCTATGGAAGTATGGGAAACGCCGCTCCACA 1040

1041 ACAACGTATCGTTGCTCAACTAGGTCAGGGTGTCTACAGA 1080
5 1081 ACCTTGTCTTCCACCTTGTACAGAAGACCCTTCAATATCG 1120
1121 GTATCAACAACCAGCAACTTTCGGTTCTTGACGGAACAGA 1160
1161 GTTCGCCTATGGAACCTCTTCTAACTTGCCATCCGCTGTT 1200
10 1201 TACAGAAAGAGCGGAACCGTTGATTCCTTGGACGAAATCC 1240
1241 CACCACAGAACAACAATGTGCCACCCAGGCAAGGATTCTC 1280
15 1281 CCACAGGTTGAGCCACGTGTCCATGTTCCGTTCCGGATTTC 1320
1321 AGCAACAGTTCCGTGAGCATCATCAGAGCTCCTATGTTCT 1360
1361 CATGGATTTCATCGTAGTGCTGAGTTCAACAATATCATTCC 1400
20 1401 TTCCTCTCAAATCACCCAAATCCCATTGACCAAGTCTACT 1440
1441 AACCTTGATCTGGAACCTCTGTCGTGAAAGGACCAGGCT 1480
1481 TCACAGGAGGTGATATTCTTAGAAGAACTTCTCCTGGCCA 1520
25 1521 GATTAGCACCTCAGAGTTAACATCACTGCACCACTTTCT 1560
1561 CAAAGATATCGTGTGTCAGGATTCGTTACGCATCTACCACTA 1600
30 1601 ACTTGCAATTCCACACCTCCATCGACGGAAGGCCTATCAA 1640

	1641	TCAGGGTAACTTCTCCGCAACCATGTCAAGCGGCAGCAAC	1680
5	1681	TTGCAATCCGGCAGCTTCAGAACCGTCGGTTTCACTACTC	1720
	1721	CTTTCAACTTCTCTAACGGATCAAGCGTTTTCCACCCTTAG	1760
	1761	CGCTCATGTGTTCAATTCTGGCAATGAAGTGACATTGAC	1800
10	1801	CGTATTGAGTTTGTGCCTGCCGAAGTTACCCTCGAGGCTG	1840
	1841	AGTACAACCTTGAGAGAGCCAGAAGGCTGTGAACGCCCT	1880
15	1881	CTTTACCTCCACCAATCAGCTTGGCTTGAAAATAACGTT	1920
	1921	ACTGACTATCACATTGACCAAGTGTCCAAGTTGGTCACCT	1960
	1961	ACCTTAGCGATGAGTTCTGCTCGACGAGAAGCGTGAAGT	2000
20	2001	CTCCGAGAAAGTTAAACACGCCAAGCGTCTCAGCGACGAG	2040
	2041	AGGAATCTCTTGCAAGACTCCAAGTTCAAAGACATCAACA	2080
	2081	GGCAGCCAGAACGTGGTTGGGGTGAAGCACCAGGATCAC	2120
25	2121	CATCCAAGGAGGCGACGATGTGTTCAAGGAGAACTACGTC	2160
	2161	ACCCTCTCCGGAAGTTTCGACGAGTGCTACCCTACCTACT	2200
30	2201	TGTACCAGAAGATCGATGAGTCCAAACTCAAAGCCTTCAC	2240

2241 CAGGTATCAACTTAGAGGCTACATCGAAGACAGCCAAGAC 2280
5 2281 CTTGAAATCTACTCGATCAGGTACAATGCCAAGCACGAGA 2320
2321 CCGTGAATGTCCCAGGTACTGGTTCCCTCTGGCCACTTTC 2360
2361 TGCCCAATCTCCCATTGGGAAGTGTGGAGAGCCTAACAGA 2400
10 2401 TGCCTCCACACCTTGAGTGGAATCCTGACTTGGAAGTCT 2440
2441 CCTGCAGGGATGGCGAGAACTGTGCCCACCATCTCATCA 2480
15 2481 CTTCTCCTTGGACATCGATGTGGGATGTACTGACCTGAAT 2520
2521 GAGGACCTCGGAGTCTGGGTATCTTCAAGATCAAGACCC 2560
2561 AAGACGGACACGCAAGACTTGGCAACCTTGAGTTTCTCGA 2600
20 2601 AGAGAAACCATTGGTCGGTGAAGCTCTCGCTCGTGTGAAG 2640
2641 AGAGCAGAGAAGAAGTGGAGGGACAAACGTGAGAACTCG 2680
2681 AATGGGAAACTAACATCGTTTACAAGGAGGCCAAAGAGTC 2720
25 2721 CGTGGATGCTTTGTTCTGTGAAGTCCCAATATGATCAGTTG 2760
2761 CAAGCCGACACCAACATCGCATGATCCACGCCGAGACA 2800
30 2801 AACGTGTGCACAGCATTCGTGAGGCTTACTTGCCTGAGTT 2840

2841 GTCCGTGATCCCTGGTGTGAACGCTGCCATCTTCGAGGAA 2880
5 2881 CTTGAGGGACGTATCTTTACCGCATTCTCCTGTACGATG 2920
2921 CCAGAAACGTCATCAAGAACGGTGACTTCAACAATGGCCT 2960
2961 CAGCTGCTGGAATGTGAAAGGTCATGTGGACGTGGAGGAA 3000
10 3001 CAGAACAATCAGCGTTCGGTCTGGTTGTGCCTGAGTGGG 3040
3041 AAGCTGAAGTGTCCCAAGAGGTTAGAGTCTGTCCAGGTAG 3080
15 3081 AGGCTACATTCTCCGTGTGACCGCTTACAAGGAGGGATAC 3120
3121 GGTGAGGGTTGCGTGACCATCCACGAGATCGAGAACAACA 3160
3161 CCGACGAGCTTAAGTTCTCCAAGTGCCTCGAGGAAGAAAT 3200
20 3201 CTATCCCAACAACACCGTTACTTGCAACGACTACACTGTG 3240
3241 AATCAGGAAGAGTACGGAGGTGCCTACACTAGCCGTAACA 3280
3281 GAGGTTACAACGAAGCTCCTTCCGTTCCCTGCTGACTATGC 3320
25 3321 CTCCGTGTACGAGGAGAAATCCTACACAGATGGCAGACGT 3360
3361 GAGAACCCTTGCGAGTTCAACAGAGGTTACAGGGACTACA 3400
30 3401 CACCACTTCCAGTTGGCTATGTTACCAAGGAGCTTGAGTA 3440

3441 CTTTCCTGAGACCGACAAAGTGTGGATCGAGATCGGTGAA 3480
 5 3481 ACCGAGGGAACCTTCATCGTGGACAGCGTGGAGCTTCTCT 3520
 3521 TGATGGAGGAA 3531

27. A method of Claim 4 further comprising removal
 10 of sequences comprising more than five consecutive A+T
 or G+C bases.

28. A structural gene sequence of Claim 13
 comprising a majority of plant preferred codons.

29. A structural gene encoding the coat protein of
 15 potato leaf roll virus, said gene having the sequence:

1 ATGAGTACTGTCGTGGTTAAGGGAAACGTGAACGGTGGTG 40
 41 TTCAACAACCTAGAGGAGAAGAAGGCAATCCCTTCGTAG 80
 20 81 GAGAGCTAACAGAGTTCAGCCAGTGGTTATGGTCACTGCT 120
 121 CCTGGGCAACCAAGAAGGAGAAGAAGGAGAAGAGGAGGTA 160
 161 ATCGCAGATCAAGAAGAACTGGAGTCCCAGAGGAAGAGG 200
 25 201 TTCAAGCGAGACATTCGTGTTTACAAAGGACAACCTCGTG 240
 241 GGCAACTCCCAAGGAAGTTTCACCTTCGGACCAAGTGTTT 280
 30 281 CAGACTGTCCAGCATTCAAGGATGGAATACTCAAGGCTTA 320

5 321 CCATGAGTACAAGATCACAAGTATCTTGCTTCAGTTCGTC 360

361 AGCGAGGCCTCTTCCACCTCTCCAGGCTCCATCGCTTATG 400

401 AGTTAGATCCACATTGCAAAGTTTCATCCCTCCAGTCCTA 440

10 441 CGTCAACAAGTTCCAAATCACAAGGGTGGTGCTAAGACC 480

481 TATCAAGCTCGTATGATCAACGGAGTTGAATGGCACGATT 520

521 CTTCTGAGGATCAGTGCAGAAATCCTTTGGAAAGGAAATGG 560

15 561 AAAGTCTTCAGATCCAGCTGGATCTTTCAGAGTTACCATC 600

601 AGAGTTGCTCTTCAAAACCCAAAAG 624.

20 30. A chimeric plant gene which comprises a structural coding sequence encoding an insecticidal protein of *Bacillus thuringiensis*, said structural coding sequence being modified to reduce the number of putative polyadenylation signals within said structural coding sequence.

25 31. A chimeric plant gene of Claim 30 in which the polyadenylation signals are selected from the group consisting of AATAAA, AATAAT, AACCAA, ATATAA, AATCAA, ATACTA, ATAAAA, ATGAAA, AAGCAT, ATTAAT, ATACAT, AAAATA, ATTAAA, AATTAA, AATACA and CATAAA.

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32. A chimeric plant gene of Claim 31 in which said structural coding sequence is further modified to reduce the number of ATTTA sequences within said structural coding sequence.

33. A chimeric plant gene of Claim 32 in which said structural coding sequence is substantially devoid of polyadenylation signals and ATTTA sequences.

34. A transformed plant cell containing a gene of Claim 33.

35. A transformed plant cell of Claim 34 selected from the group consisting of soybean, cotton, alfalfa, oilseed rape, flax, tomato, sugarbeet, sunflower, potato, tobacco, maize, rice and wheat.

36. A plant comprising transformed plant cells of Claim 34.

37. A plant of Claim 36 which comprises plant cells of Claim 35.

38. A seed produced by a plant of Claim 36.

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